

## SEARCH NOTES

14 JUN 02

**09/899,082**

Databases searched: USPATFULL via EAST, Caplus, Medline, Biosis

Reviewed Parent Application(s) : 09/378,900 and 09/044,665

### **Search terms:**

Inventor(s) : e.g. Maertens G?/au

STIC searched SEQ ID NOs : 1-4, 20 and 27

HCV

Hybridization

Amplification or PCR

*Good Out*

**SEQ ID NO: 1**

RESULT 5  
I73300  
LOCUS I73300 51 bp DNA linear PAT  
03-APR-1998  
DEFINITION Sequence 31 from patent US 5686272.  
ACCESSION I73300  
VERSION I73300.1 GI:3009439  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.  
TITLE Amplification of RNA sequences using the ligase chain reaction  
JOURNAL Patent: US 5686272-A 31 11-NOV-1997;  
FEATURES Location/Qualifiers  
source 1..51  
/organism="unknown"  
BASE COUNT 14 a 16 c 10 g 11 t  
ORIGIN

Query Match 98.5%; Score 26.6; DB 6; Length 51;  
Best Local Similarity 96.3%; Pred. No. 0.036;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps  
0;

Qy 1 CCCTGTGAGGAACTWCTGTCTTCACGC 27  
|||||||:|||||||  
Db 16 CCCTGTGAGGAACTACTGTCTTCACGC 42

# SEQ ID NO: 1

RESULT 15

AAA75294

ID AAA75294 standard; cDNA; 308 BP

AC AAA75294;

DT 15-JAN-2001 (first entry)

DE Novel hepatitis C virus cDNA clone 18g.

KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;

KW viral infectivity; viral replication; ds.

XX

OS Hepatitis C virus.

XX

PN EP1034785-A2.

XX

PD 13-SEP-2000.

XX

PF 16-MAR-1990; 2000EP-0109602.

XX

PR 17-MAR-1989; 89US-0325338.

PR 20-APR-1989; 89US-0341334.

PR 18-MAY-1989; 89US-0355002.

PR 16-MAR-1990; 90EP-0302866.

XX

PA (CHIR ) CHIRON CORP.

XX

PI Houghton M, Choo Q, Kuo G;

XX

DR WPI; 2000-566891/53.

XX

PT Novel composition comprising a hepatitis C virus antisense

PT polynucleotide which is complementary to or corresponds to a sense

PT strand of the virus genome, and selectively hybridises to it -

XX

PS Example; Fig 14; 75pp; English.

XX

CC The specification describes a pharmaceutical composition which  
CC comprises a hepatitis C virus (HCV) antisense polynucleotide. The  
CC HCV is characterized by a positive stranded RNA genome which has  
CC 40% homology at the polypeptide level to a HCV polyprotein. The  
CC antisense polynucleotide binds to cellular polynucleotides which  
CC enhance and/or are required for viral infectivity, replicative  
CC ability or chronicity. The antisense polynucleotides may also be  
CC designed to bind with high specificity, to be of increased stability,  
CC to be stable and to have low toxicity. The composition also comprises  
CC an agent which causes viral RNA to be inactive. The composition  
CC is used for preventing HCV replication in a system. The present  
CC sequence represents a novel HCV cDNA sequence, which is used in the  
CC course of the invention.

XX

SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 other;

Query Match 98.5%; Score 26.6; DB 21; Length 308;  
Best Local Similarity 96.3%; Pred. No. 0.011;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps  
0;

Qy 1 CCCTGTGAGGAACTWCTGTCTTCACGC 27  
|||:|||||  
Db 19 ccctgtgaggaaactactgtcttcacgc 45

# SEQ ID NO: 1

RESULT 9  
HPCBR56A  
LOCUS HPCBR56A 296 bp RNA linear VRL  
03-FEB-1999  
DEFINITION Hepatitis C virus RNA, 5'untranslated region.  
ACCESSION D13448  
VERSION D13448.1 GI:435625  
KEYWORDS 5' untranslated region.  
SOURCE Hepatitis C virus (isolate:BR56) cDNA to genomic RNA.  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Flaviviridae;  
Hepacivirus.  
  
REFERENCE 2 (sites)  
AUTHORS Bukh,J., Purcell,R.H. and Miller,R.H.  
TITLE Sequence analysis of the 5' noncoding region of hepatitis C virus  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)  
MEDLINE 92279243  
FEATURES Location/Qualifiers  
source 1. .296  
/organism="Hepatitis C virus"  
/isolate="BR56"  
/db\_xref="taxon:11103"  
BASE COUNT 53 a 88 c 94 g 61 t  
ORIGIN

Query Match 98.5%; Score 26.6; DB 14; Length 296;  
Best Local Similarity 96.3%; Pred. No. 0.027;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps  
0;

Qy 1 CCCTGTGAGGAAGTCTGTCTTCACGC 27  
|||||||:|||||||  
Db 6 CCCTGTGAGGAAGTCTGTCTTCACGC 32

Had And

## SEQ ID NO: 2

RESULT 2

AAQ85918

ID AAQ85918 standard; DNA; 21 BP.

XX

AC AAQ85918;

XX

DT 02-NOV-1995 (first entry)

XX

DE Hepatitis C virus genome external PCR primer YK-104.

XX

KW Hepatitis C virus; HCV; non-A non-B; external PCR primer;

KW YK-104; primer specific detection; ss.

XX

OS Synthetic.

XX

PN WO9506753-A.

XX

PD 09-MAR-1995.

XX

PF 02-SEP-1994; 94WO-US09869.

XX

PR 03-SEP-1993; 93US-0116344.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Fields HA, Khudyakov YE;

XX

DR WPI; 1995-115465/15.

XX

PT New method and kit for primer-specific detection of nucleic acids

PT - using two primers having a known sequence and a marker, resp

PT for solid-phase detection of amplification prods.

XX

PS Example 1; Page 11; 20pp; English.

XX

CC AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for

CC the Hepatitis C virus (HCV) genome. They were used to demonstrate

CC a new method for the primer specific detection of nucleic acids.

XX

SQ Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 21; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACGGTCTACGAGACCT 21

||||||||||||||||

Db 1 ggtgcacggtctacgagacct 21

## SEQ ID NO: 2

RESULT 6

AAQ67081

ID AAQ67081 standard; DNA; 25 BP.

XX

AC AAQ67081;

XX

DT 14-MAR-1995 (first entry)

XX

DE Antisense primer for amplifying Hepatitis C virus DNA fragment.

XX

KW Hepatitis C virus; restriction endonuclease; KpnI; marker;  
KW cleavage site; HCV; ss.

XX

OS Synthetic.

XX

PN JP06181764-A.

XX

PD 05-JUL-1994.

XX

PF 20-JAN-1993; 93JP-0007721.

XX

PR 22-SEP-1992; 92JP-0252793.

XX

PA (SAKA ) OTSUKA PHARM CO LTD.

XX

DR WPI; 1994-251687/31.

XX

PT DNA contg. KPNI recognition site as marker for hepatitis C virus

PT - useful in diagnosis of HC

XX

PS Disclosure; Page 8; 9pp; Japanese.

XX

CC Two primers (AAQ67080, AAQ67081) were used to amplify the sequence  
CC described in AAQ67079 which is obtained from hepatitis C virus (HCV)

CC and comprises a KpnI restriction endonuclease recognition site.

CC The restriction site is found in the wild type sequence and can

CC therefore be used as a diagnostic marker.

XX

SQ Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACGGTCTACGAGACCT 21

||||||||||||||||||||

Db 3 ggtgcacggtctacgagacct 23

## SEQ ID NO: 2

RESULT 5

US-08-441-971-33/c

; Sequence 33, Application US/08441971

; Patent No. 6071693

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS Version 3.3

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,971

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/221,653

; FILING DATE:

; APPLICATION NUMBER: US/07/881,528

; FILING DATE:

; APPLICATION NUMBER: 07/697,326

; FILING DATE: 8 May 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Janiuk, Anthony J.

; REGISTRATION NUMBER: 29,809

; REFERENCE/DOCKET NUMBER: C0772/7000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 720-3500

; TELEFAX: (617) 720-2441

; TELEX: EZEKIEL

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; ORIGINAL SOURCE: (ATCC # 40394)

; INDIVIDUAL ISOLATE: hcv1

US-08-441-971-33

Query Match 100.0%; Score 21; DB 3; Length 252;

Best Local Similarity 100.0%; Pred. No. 0.052;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACGGTCTACGAGACCT 21

|||||||

Db 252 GGTGCACGGTCTACGAGACCT 232

## SEQ ID NO: 2

RESULT 9  
AAQ43112  
ID AAQ43112 standard; DNA; 29 BP.  
XX  
AC AAQ43112;  
XX  
DT 23-SEP-1993 (first entry)  
XX  
DE HCV 5'NCR antisense primer 209.  
XX  
KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1;  
KW HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3;  
KW PCR; amplify; polymerase chain reaction; primer; NS4; ss.  
XX  
OS Synthetic.  
XX  
PN WO9310239-A.  
XX  
PD 27-MAY-1993.  
XX  
PF 20-NOV-1992; 92WO-GB02143.  
XX  
PR 21-NOV-1991; 91GB-0024696.  
PR 24-JUN-1992; 92GB-0013362.  
XX  
PA (COMM-) COMMON SERVICES AGENCY.  
XX  
PI Chan S, Simmonds P, Yap PL;  
XX  
DR WPI; 1993-182554/22.  
XX  
PT DNA encoding antigenic peptide(s) of new types of hepatitis C  
PT virus - for diagnosing and treating HCV infection, screening  
PT blood samples and identifying different HCV types  
XX  
PS Disclosure; Page 27; 120pp; English.  
XX  
CC The sequences given in AAQ43112-33 are primers which were used to  
CC amplify specific regions of the hepatitis C virus (HCV) genome.  
CC Analysis of regions of the HCV genome revealed the existence of  
CC three distinct groups of HCV. Analysis of the region encompassing  
CC -255 to -62 of the 5' non coding region (NCR) (see AAQ43058-75) showed  
CC a difference of 9-14% in the nucleotide sequences between the three  
CC groups. Two of the groups identified were similar to those of HCV  
CC variants termed type 1 and 2, whilst the third appeared to represent  
CC a novel type of virus. Comparison of the NS3 region (see AAR37927-30)  
CC showed a high degree of sequence diversity with type 3 being phylo-  
CC genetically different to type 1 and 2. The same degree different-  
CC iation was noted in the NS-5 (see AAR37923-26), core region (see  
CC AAR37931) and the NS4 region (see AAQ43106-111) between type 3 and type  
CC 1 sequences.  
XX  
SQ Sequence 29 BP; 7 A; 8 C; 8 G; 6 T; 0 other;  
Query Match 100.0%; Score 21; DB 14; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTGCACGGTCTACGAGACCT 21  
|||  
Db 9 ggtgcacggtctacgagacct 29